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Sequence Listing was accepted.

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Reviewer: Anne Corrigan

Timestamp: [year=2008; month=3; day=3; hr=13; min=34; sec=18; ms=439;]

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Application No: 10615668 Version No: 2.0

Input Set:

Output Set:

Started: 2008-02-19 13:46:11.440
Finished: 2008-02-19 13:46:12.579
Elapsed: 0 hr(s) 0 min(s) 1 sec(s) 139 ms
Total Warnings: 3
Total Errors: 0
No. of SeqIDs Defined: 29
Actual SeqID Count: 29

Error code	Error Description
W 213	Artificial or Unknown found in <213> in SEQ ID (1)
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W 402	Undefined organism found in <213> in SEQ ID (29)

SEQUENCE LISTING

<110> Covacci, Antonio
Bugnoli, Massimo
Telford, John
Macchia, Giovanni
Rappuoli, Rino

<120> HELICOBACTER PYLORI CAI ANTIGEN POLYNUCLEOTIDES

<130> CHIR-0213

<140> 10615668

<141> 2003-07-08

<150> US 09/410,835

<151> 1999-10-01

<150> US 08/471,491

<151> 1995-06-06

<150> US 08/256,848

<151> 1994-10-21

<160> 29

<170> PatentIn version 3.3

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<223> primer oligonucleotide

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<213> Helicobacter pylori

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 35 40 45

Ala Thr Gly Thr Ala Val Gly Thr Val Ser Gly Leu Leu Ser Trp Gly
 50 55 60

Leu Lys Gln Ala Glu Glu Ala Asn Lys Thr Pro Asp Lys Pro Asp Lys
 65 70 75 80

Val Trp Arg Ile Gln Ala Gly Lys Gly Phe Asn Glu Phe Pro Asn Lys
 85 90 95

Glu Tyr Asp Leu Tyr Arg Ser Leu Leu Ser Ser Lys Ile Asp Gly Gly
 100 105 110

Trp Asp Trp Gly Asn Ala Ala Arg His Tyr Trp Val Lys Gly Gly Gln
 115 120 125

Gln Asn Lys Leu Glu Val Asp Met Lys Asp Ala Val Gly Thr Tyr Thr
 130 135 140

Leu Ser Gly Leu Arg Asn Phe Thr Gly Gly Asp Leu Asp Val Asn Met
 145 150 155 160

Gln Lys Ala Thr Leu Arg Leu Gly Gln Phe Asn Gly Asn Ser Phe Thr

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Ser Gly Ala Gly Arg Lys Ala Ser Ser Thr Val Leu Thr Leu Gln Ala		
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Ser Glu Gly Ile Thr Ser Asp Lys Asn Ala Glu Ile Ser Leu Tyr Asp		
225	230	235 240
Gly Ala Thr Leu Asn Leu Ala Ser Ser Ser Val Lys Leu Met Gly Asn		
245	250	255
Val Trp Met Gly Arg Leu Gln Tyr Val Gly Ala Tyr Leu Ala Pro Ser		
260	265	270
Tyr Ser Thr Ile Asn Thr Ser Lys Val Thr Gly Glu Val Asn Phe Asn		
275	280	285
His Leu Thr Val Gly Asp Lys Asn Ala Ala Gln Ala Gly Ile Ile Ala		
290	295	300
Asn Lys Lys Thr Asn Ile Gly Thr Leu Asp Leu Trp Gln Ser Ala Gly		
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Leu Asn Ile Ile Ala Pro Pro Glu Gly Gly Tyr Lys Asp Lys Pro Asn		
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Asn Thr Pro Ser Gln Ser Gly Ala Lys Asn Asp Lys Asn Glu Ser Ala		
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Lys Asn Asp Lys Gln Glu Ser Ser Gln Asn Asn Ser Asn Thr Gln Val		
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Ile Asn Pro Pro Asn Ser Ala Gln Lys Thr Glu Val Gln Pro Thr Gln		
370	375	380
Val Ile Asp Gly Pro Phe Ala Gly Gly Lys Asp Thr Val Val Asn Ile		
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Lys Ala Ser Leu Thr Thr Asn Ala Ala His Leu His Ile Gly Lys Gly
420 425 430

Gly Val Asn Leu Ser Asn Gln Ala Ser Gly Arg Ser Leu Ile Val Glu
435 440 445

Asn Leu Thr Gly Asn Ile Thr Val Asp Gly Pro Leu Arg Val Asn Asn
450 455 460

Gln Val Gly Gly Tyr Ala Leu Ala Gly Ser Ser Ala Asn Phe Glu Phe
465 470 475 480

Lys Ala Gly Thr Asp Thr Lys Asn Gly Thr Ala Thr Phe Asn Asn Asp
485 490 495

Ile Ser Leu Gly Arg Phe Val Asn Leu Lys Val Asp Ala His Thr Ala
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Asn Phe Lys Gly Ile Asp Thr Gly Asn Gly Gly Phe Asn Thr Leu Asp
515 520 525

Phe Ser Gly Val Thr Asp Lys Val Asn Ile Asn Lys Leu Ile Thr Ala
530 535 540

Ser Thr Asn Val Ala Val Lys Asn Phe Asn Ile Asn Glu Leu Ile Val
545 550 555 560

Lys Thr Asn Gly Ile Ser Val Gly Glu Tyr Thr His Phe Ser Glu Asp
565 570 575

Ile Gly Ser Gln Ser Arg Ile Asn Thr Val Arg Leu Glu Thr Gly Thr
580 585 590

Arg Ser Leu Phe Ser Gly Gly Val Lys Phe Lys Gly Gly Glu Lys Leu
595 600 605

Val Ile Asp Glu Phe Tyr Tyr Ser Pro Trp Asn Tyr Phe Asp Ala Arg
610 615 620

Asn Ile Lys Asn Val	Glu Ile Thr Asn Lys	Leu Ala Phe Gly Pro Gln
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Gly Ser Pro Trp Gly Thr Ser Lys	Leu Met Phe Asn Asn	Leu Thr Leu
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Gly Gln Asn Ala Val Met Asp Tyr	Ser Gln Phe Ser Asn	Leu Thr Ile
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Gln Gly Asp Phe Ile Asn Asn Gln	Gly Thr Ile Asn Tyr	Leu Val Arg
675	680	685
Gly Gly Lys Val Ala Thr Leu Ser Val	Gly Asn Ala Ala Ala Met Met	
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Phe Asn Asn Asp Ile Asp Ser Ala Thr	Gly Phe Tyr Lys Pro Leu Ile	
705	710	715 720
Lys Ile Asn Ser Ala Gln Asp Leu Ile	Lys Asn Thr Glu His Val Leu	
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Leu Lys Ala Lys Ile Ile Gly Tyr	Gly Asn Val Ser Thr Gly Thr Asn	
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Gly Ile Ser Asn Val Asn Leu Glu Glu	Gln Phe Lys Glu Arg Leu Ala	
755	760	765
Leu Tyr Asn Asn Asn Asn Arg Met Asp	Thr Cys Val Val Arg Asn Thr	
770	775	780
Asp Asp Ile Lys Ala Cys Gly Met Ala	Ile Gly Asp Gln Ser Met Val	
785	790	795 800
Asn Asn Pro Asp Asn Tyr Lys Tyr Leu	Ile Gly Lys Ala Trp Lys Asn	
805	810	815
Ile Gly Ile Ser Lys Thr Ala Asn Gly	Ser Lys Ile Ser Val Tyr Tyr	
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Leu Gly Asn Ser Thr Pro Thr Glu Asn	Gly Gly Asn Thr Thr Asn Leu	
835	840	845

Pro Thr Asn Thr Thr Ser Asn Ala Arg Ser Ala Asn Asn Ala Leu Ala
850 855 860

Gln Asn Ala Pro Phe Ala Gln Pro Ser Ala Thr Pro Asn Leu Val Ala
865 870 875 880

Ile Asn Gln His Asp Phe Gly Thr Ile Glu Ser Val Phe Glu Leu Ala
885 890 895

Asn Arg Ser Lys Asp Ile Asp Thr Leu Tyr Ala Asn Ser Gly Ala Gln
900 905 910

Gly Arg Asp Leu Leu Gln Thr Leu Leu Ile Asp Ser His Asp Ala Gly
915 920 925

Tyr Ala Arg Lys Met Ile Asp Ala Thr Ser Ala Asn Glu Ile Thr Lys
930 935 940

Gln Leu Asn Thr Ala Thr Thr Thr Leu Asn Asn Ile Ala Ser Leu Glu
945 950 955 960

His Lys Thr Ser Gly Leu Gln Thr Leu Ser Leu Ser Asn Ala Met Ile
965 970 975

Leu Asn Ser Arg Leu Val Asn Leu Ser Arg Arg His Thr Asn His Ile
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995 1000 1005

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Tyr Glu Lys Pro Thr Asn Val Trp Ala Asn Ala Ile Gly Gly Thr
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Ala Thr Arg Ala Ser Tyr Gly Tyr Asp Phe Ala Phe Phe Arg Asn				
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